

SEQUENCE LISTING

<110> Chandrashekar, Ramaswamy
Morales, Tony H.

<120> Parasitic Helminth Cuticlin Proteins, Nucleic Acid
Molecules, and Uses Thereof

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<140> not yet assigned

<141> 1999-06-01

<150> 60/087,435

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<170> PatentIn Ver. 2.0

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acc att aaa gaa cca aat agc gaa tgt gtt cga cca caa tgt tca gaa 816
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 195 200 205

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<213> *Dirofilaria immitis*

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 1 5 10 15

Val Ser Glu Met Thr Thr Ala Phe Gln Thr Gln Val Val Pro Met Pro
 20 25 30

Val Cys Arg Tyr Glu Ile Leu Glu Gly Gly Pro Thr Gly Ala Pro Val
 35 40 45

Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp
 50 55 60

Ser Glu Thr Thr Asp Thr Phe Cys Ala Leu Val His Ser Cys Val Val
 65 70 75 80

Asp Asp Gly Lys Gly Asp Ala Val Glu Ile Leu Asn Glu Glu Gly Cys
 85 90 95

Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu
 100 105 110

Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu
 115 120 125

Leu Tyr Tyr Gln Cys Gln Ile Ser Ile Thr Ile Lys Glu Pro His Ser
 130 135 140

Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile
 145 150 155 160

Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala
 165 170 175

Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile
 180 185 190

Asn Ser Asp Asn Thr Val Asp Val Ser Thr Gly Phe Ser Thr Val Asp
 195 200 205

Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser
 210 215 220

Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp
 225 230 235 240

Ile Leu Leu Ile Ile Leu Phe Gly Ala Met Leu Ala Ile Ala Cys Ile
 245 250 255

Phe Phe Thr Ala Phe Leu Val His Ser Asn Asn His Ser Lys Ser
 260 265 270

<210> 10

<211> 813

<212> DNA

<213> *Dirofilaria immitis*

<400> 10

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 taacatagca ccgaacaaaa tgataagtaa aatatcattt gatgcaatac agaagatacc 120
 attgaattgt tcacggctcg ttgatgatga taaacgattt gctgagaagt tcggattctc 180
 ttcggttata tcaaccgtgc taaaaccgggt actgacgtcc accgtattat cagaattaat 240
 tgatcgcttc ttgatcaatc gtggagaaag caaggaagct tctggagctg gtgcagcagc 300
 agattttaca gcagcaaata cttgtccaga ttttatggca ccaaatacctt gtggctctgt 360
 gcattgtggt cgaggacatt cgctatgtgg ctctttaatt gttatactaa tctggcattg 420
 atagtaaagt tctgatcgat ctgcatattt ataaacatga gcttcttggc cagccattaa 480
 atctgtaata tattccaaat tattgagtaa atatttgtcc aaagcacatc cttcttcatt 540
 cagaatctcc actgcatcac cttttccatc atccacaaca catgaatgta ctaatgcaca 600
 gaatgtatct gtagtctctg aatcacatgt ccatttgtga tatacatgat ctccaatcat 660
 tgcaaatcga acaggtgcac cagttgggtcc accttccaaa atctcatatc gacatacggg 720
 cattggtacc acttgagttt ggaatgctgt agtcatttca gatacttcaa ggaccagtac 780
 taacggtctt atcagctttc catataaaaa cat 813

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
ggctggccaa gaagctcacg tatacaaata tgcg

34

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
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34

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
ggtttaatta cccaagtttg ag

22

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
ccatcctaatacgcactcactatagggc

27

<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15
ggttatatcaaccgtgctaa aaccgggtactgacgtccaccg

41

<210> 16
<211> 892
<212> DNA
<213> Brugia malayi

<220>
<221> CDS
<222> (158)..(892)

<400> 16
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gcaatttcaa attaatacatt ttgctaattc tattattcca actattttca tcaactaatca 120
ctgagaagaa atcaggaaga aagaagcaaa aagttaa atg ttg cat atg caa att 175
Met Leu His Met Gln Ile
1 5

tgc tca ttt ttg tca tat atg ata ata gca agt att aat gct att cca 223
Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala Ser Ile Asn Ala Ile Pro
10 15 20

att gat aat ggt gtc gaa agt gaa cct gaa att gaa tgt ggt cca aca 271
Ile Asp Asn Gly Val Glu Ser Glu Pro Glu Ile Glu Cys Gly Pro Thr
25 30 35

tca atc act gtt aat ttt aat act cga aat cct ttt gaa gga cat gta 319
Ser Ile Thr Val Asn Phe Asn Thr Arg Asn Pro Phe Glu Gly His Val
40 45 50

tat gct aaa gga tta tac agt aat caa gat tgt cgt agt gat gaa ggt 367

Tyr	Ala	Lys	Gly	Leu	Tyr	Ser	Asn	Gln	Asp	Cys	Arg	Ser	Asp	Glu	Gly		
55					60					65					70		
gga cgt cag gta gcc gga ata tca tta ccg ttt gat tca tgt aat gtc 415																	
Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp Ser Cys Asn Val																	
				75				80						85			
gca cgt aca cgt tcg tta aat cca cgt gga ata ttt gtc aca gct gtt 463																	
Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe Val Thr Ala Val																	
				90				95						100			
gtg gta att acg ttt cat cca cag ttt atc aca aaa gtt gat cga aca 511																	
Val Val Ile Thr Phe His Pro Gln Phe Ile Thr Lys Val Asp Arg Thr																	
				105				110						115			
tat cga ttg caa tgc ttt tac atg gaa gct gat aag act gtt agc aca 559																	
Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala Asp Lys Thr Val Ser Thr																	
				120				125						130			
caa att gaa gtt tcc gaa atg aca acc gta ttt gct aca caa ttg gta 607																	
Gln Ile Glu Val Ser Glu Met Thr Thr Val Phe Ala Thr Gln Leu Val																	
				135				140						145			150
cca atg cct gtg tgt aga tat gag att ctg gat ggt ggt cca acc gga 655																	
Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly Gly Pro Thr Gly																	
				155				160						165			
caa cct gtc cag tat gct aat att gga caa ccg gtt tat cat aaa tgg 703																	
Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln Pro Val Tyr His Lys Trp																	
				170				175						180			
aca tgt gat tct gaa aca gtt gat acc ttc tgt gct ttg gta cat tcc 751																	
Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala Leu Val His Ser																	
				185				190						195			
tgt ttt gtt gat gat ggc aat ggt gac agt att aat tta att aat gaa 799																	
Cys Phe Val Asp Asp Gly Asn Gly Asp Ser Ile Asn Leu Ile Asn Glu																	
				200				205						210			
gaa gga tgt gca tta gat cga tat ctt cta aat aat ttg gaa tat cca 847																	
Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu Asn Asn Leu Glu Tyr Pro																	
				215				220						225			230
act gat cta atg gct ggc caa gaa gct cac gta tac aaa tat gcg 892																	
Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala																	
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<210> 17

<211> 245

<212> PRT

<213> Brugia malayi

<400> 17

Met Leu His Met Gln Ile Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala
1 5 10 15

Ser Ile Asn Ala Ile Pro Ile Asp Asn Gly Val Glu Ser Glu Pro Glu
20 25 30

Ile Glu Cys Gly Pro Thr Ser Ile Thr Val Asn Phe Asn Thr Arg Asn
35 40 45

Pro Phe Glu Gly His Val Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp
50 55 60

Cys Arg Ser Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro
65 70 75 80

Phe Asp Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly
85 90 95

Ile Phe Val Thr Ala Val Val Val Ile Thr Phe His Pro Gln Phe Ile
100 105 110

Thr Lys Val Asp Arg Thr Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala
115 120 125

Asp Lys Thr Val Ser Thr Gln Ile Glu Val Ser Glu Met Thr Thr Val
130 135 140

Phe Ala Thr Gln Leu Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu
145 150 155 160

Asp Gly Gly Pro Thr Gly Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln
165 170 175

Pro Val Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe
180 185 190

Cys Ala Leu Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Ser
195 200 205

Ile Asn Leu Ile Asn Glu Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu
210 215 220

Asn Asn Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His
 225 230 235 240

Val Tyr Lys Tyr Ala
 245

<210> 18
 <211> 892
 <212> DNA
 <213> Brugia malayi

<400> 18
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 atttagaaga tatcgatcta atgcacatcc ttcttcatta attaaattaa tactgtcacc 120
 attgccatca tcaacaaaac aggaatgtac caaagcacag aaggtatcaa ctgtttcaga 180
 atcacatgtc catttatgat aaaccggttg tccaatatta gcatactgga caggttgtcc 240
 gggttgacca ccatccagaa tctcatatct acacacagga attggtacca attgtgtagc 300
 aaatacgggt gtcatttcgg aaacttcaat ttgtgtgcta acagtcttat cagcttccat 360
 gtaaaagcat tgcaatcgat atgttogatc aacttttgtg ataaactgtg gatgaaacgt 420
 aattaccaca acagctgtga caaatattcc acgtggattt aacgaacgtg tacgtgcgac 480
 attacatgaa tcaaacggta atgatattcc ggctacctga cgtccacctt catcactacg 540
 acaatcttga ttactgtata atccttttagc atatacatgt ccttcaaaag gatttcgagt 600
 attaaaatta acagtgattg atgttggacc acattcaatt tcaggttcac ttctgacacc 660
 attatcaatt ggaatagcat taatacttgc tattatcata tatgacaaaa atgagcaaatt 720
 ttgcatatgc aacatttaac tttttgcttc tttcttctg atttcttctc agtgattagt 780
 gatgaaaata gttggaataa tagaattagc aaaatgatta atttgaaatt gcaacaaatt 840
 attgaattat tgatgatcaa ttttaatgat ctcaaacttg ggtaattaaa cc 892

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